

Sequence Match Listing
for 09/959987

RESULT 6
BE705670/c
LOCUS BE705670 737 bp mRNA linear EST 12-SEP-2000
DEFINITION Sc01_11a10_A Sc01_AAFC_ECORC_cold_stressed_winter_rye_seedlings
Secale cereale cDNA clone Sc01_11a10, mRNA sequence.
ACCESSION BE705670
VERSION BE705670.1 GI:10093935
KEYWORDS EST.
SOURCE rye.
ORGANISM Secale cereale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Secale.
REFERENCE 1 (bases 1 to 737)
AUTHORS Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori,
.J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
TITLE Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
JOURNAL Unpublished (2000)
COMMENT Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
OC6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
FEATURES Location/Qualifiers
source 1. .737
/organism="Secale cereale"
/cultivar="Puma (winter rye)"
/db_xref="taxon:4550"
/clone="Sc01_11a10"
/clone_lib="Sc01_AAFC_ECORC_cold_stressed_winter_rye_seedlings"
/tissue_type="leaf, crown"
/dev_stage="seedling three-leaf stage"
/note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI;
Site_2: Xho I; Sampled three-leaf seedlings treated for
one week at 20°C, 12 hrs light/day. Library made with
Stratagene UNIZAP XR Kit/Gigapack III Gold Kit. Lambda
library is amplified, then mass excised in SOLR cells."
BASE COUNT 156 a 189 c 200 g 170 t 22 others
ORIGIN
Query Match 55.1%; Score 24.8; DB 12; Length 737;
Best Local Similarity 80.6%; Pred. No. 46;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CTGCATGGAGTGCGGCCAAAGTCCCTCCACCTACA 36
||| ||||| ||||||| ||| ||||| |||||
Db 549 CTGAGTGGAGGGCGCCAAGAGCCCCCTCTACTACA 514

RESULT 7

BE412777
LOCUS BE412777
DEFINITION MCG008.H03R990625 ITEC MCG Barley Leaf/Culm Library linear EST 24-JUL-2000
ACCESSION BE412777
VERSION BE412777.1 GI:9410525
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum:
REFERENCE
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,
,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogiara,Y.,
Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
Sorrells,M., Warburton,M. and Wenzel,G.
TITLE International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
JOURNAL Unpublished (2000)
COMMENT Contact: Graner A
Institute for Plant Genetics & Crop Plant Research
Corrensstr. 3, D-06466 Gatersleben GERMANY
Tel: 49 39482 5521
Fax: 49 39482 5137
Email: a_graner@ipk-gatersleben.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
FEATURES
source Location/Qualifiers
1. .928
/organism="Hordeum vulgare"
/db_xref="taxon:4513"
/clone="MCG008.H03"
/clone_lib="ITEC MCG Barley Leaf/Culm Library"
/tissue_type="leaf/culm"
/dev_stage="etiolated"
BASE COUNT 237 a 181 c 247 g 254 t 9 others
ORIGIN
Query Match 55.1%; Score 24.8; DB 10; Length 928;
Best Local Similarity 80.6%; Pred. No. 48;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 CTGCATGGAGTGGCGCCAAAGTCCCTCCACCTACA 36
Db 86 CTGAGTGGAGGGCGGCCAAGAGCCCCCTCTACTACA 121
99 104

RESULT 13
AQ984126/c
LOCUS AQ984126 503 bp DNA linear GSS 30-JAN-2000
DEFINITION RPCI-23-306D11.TV RPCI-23 Mus musculus genomic clone RPCI-23-306D11
, DNA sequence.
ACCESSION AQ984126
VERSION AQ984126.1 GI:6817331
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 503)
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-23-306D11.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Research Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 306 row: D column: 11

Seq primer: T7

Class: BAC ends.

Locat:

Location 1. . 503

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FEATURES          source          accession qualifiers
  . .503
  /organism="Mus musculus"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="RPCI-23-306D11"
  /clone_lib="RPCI-23"
  /sex="Female"
  /lab_host="DH10B"
  /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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BASE COUNT 144 a 125 c 127 g 107 t
ORIGIN

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Query Match      51.6%; Score 23.2; DB 17; Length 503;
Best Local Similarity 70.5%; Pred. No. 1.7e+02;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy 2 TGCATGGAGTGC~~GG~~CCAAAAGTCCCTCCACCTACATCCC~~G~~TAC 45

Ph 385 TAGATGCCACCCGACCCGAGACTTCTTCTCCCCACATCCGGAGAC 342

313 318

RESULT 13
T49841
hypothetical protein B24H17.270 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49841
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49841
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-218 <SCH>
A;Cross-references: EMBL AL356815, GSPDB:GN00116; NCSP:B24H17.270
A;Experimental source: BAC clone B24H17; strain OR74A
C;Genetics:
A;Gene: NCSP:B24H17.270
A;Map position: 6
A;Introns: 8/1; 107/1; 144/1; 180/2
C;Superfamily: Neurospora crassa hypothetical protein B24H17.270

Query Match 38.5%; Score 48.5; DB 2; Length 218;
Best Local Similarity 52.9%; Pred. No. 21;
Matches 9; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
Qy 3 RCDHAPNPCME-CGQKS 18
Db : || |||: ||||| 40 QADHGNEPCLPVCQKS 56

enlist date June 21 2003

RESULT 2
AF245704
LOCUS AF245704 3352 bp mRNA linear PRI 21-MAR-2001
DEFINITION Homo sapiens toll-like receptor 9 (TLR9) mRNA, complete cds.
ACCESSION AF245704
VERSION AF245704.1 GI:8575528
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3352)
AUTHORS Chuang, T.H. and Ulevitch, R.J.
TITLE Cloning and characterization of a sub-family of human toll-like receptors: hTLR7, hTLR8 and hTLR9
JOURNAL Eur. Cytokine Netw. 11 (3), 372-378 (2000)
MEDLINE 20477807
PUBMED 11022120
REFERENCE 2 (bases 1 to 3352)
AUTHORS Chuang, T.-H.H. and Ulevitch, R.J.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2000) Immunology, The Scripps Research Institute, 10550 North Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES
source Location/Qualifiers
1. .3352
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21"
/tissue_type="placenta"
gene 1. .3352
/gene="TLR9"
145. .3243
/gene="TLR9"
/codon_start=1
/product="toll-like receptor 9"
/protein_id="AAF78037.1"
/db_xref="GI:8575529"
/translation="MGFCRSALHPLSLLVQAIMLAMTIALGTLPAFLPCELQPHGLVN
CNWLFLKSVPFHMSMAAPGRNVTSLSLSSNRRIHHHLHSDFAHPLSLRHNLKWNCPVG
LSPMHFPCHMTIEPSTFLAVPTLEELNFTVSYNNIMTVPALPKSLISLSSHTNIMLDS
ASLAGLHALPFLMDGNCYKNPCRQALEVPGALLGLGNLTHLSLKYNNTVVPRNL
PSSLEYLLSYNIRIVKLAPEDLANLNTALRVLVDGGNCRRCDHAPNP CMECPRHFPLH
PDTFSHLSRLEGVLKDSSLWSWLNASWFRGLGNLRVLDLSENFLYKCITTKAFOQLT
QLRKLNLSPNYOKRVSFAHISLAPSFGSVALKEIDMHGIFFRSLDETTIPLARLPM
LQTLRLQMNFINQAOQLGIFRAPPGLRYVDSLSDNRISGASELTATMGEADGEGKVWLQP
GDLAPAPVDTPSSEDFRPNCSTLNFTLDSLRSNNLVTPQPEMFAOLSHLQCLRLSHNCI
SQAVNGSQFLPLTGLQVLDLSRNKLDDLYHEHSFTELPRLEALDLSYNSQPGMCGVGH
NFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSRLRADFSGNALGHMWAEQGDLYLHFF
QGLSGLIWLDLSQNRLHTLLPQTLLRNLPKSLQVLRDNYLAFFKWWWSLHLPKLEVL
DLAGNRLKAINTNGSLPAGTRLRRRDVSCNSISFVAPGFFSKAKELRELNLSANALKTV
DHSWFGPLASALQILDVSANPLHACGAAMDFLLEVQAAVPGPLPSRVKGSPGQLOQ
LSIFAQDRLRCLEADLSWDCFALSLLAVALGLGVPMHHLCGWDLWYCFLCLAWLPW
RGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWL
PGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLLEDRKDVVLVILS
PDGRRSRYVRLRQRLCRQSVLWPHQPSGORSFWAQLGMALTRDNHHFYNRNFCQGPT
AE"
BASE COUNT 585 a 1196 c 891 g 680 t
ORIGIN

Query Match 99.5%; Score 3080; DB 9; Length 3352;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3086; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ATGGGTTCTGCCGCAGGCCCTGCACCCGCTGTCTCTCCTGGTCAGGCCATCATGCTG 60

Db 145 ATGGGTTCTGCCGCAGGCCCTGCACCCGCTGTCTCCTGGTCAGGCCATCATGCTG 204

Qy 61 GCCATGACCCTGGCCCTGGTACCTGCCCTGCCCTACCCGTGAGCTCCAGCCCCAC 120

2003 10:03:23 23

Qy	2281 CCTCTGCACTGCGCTGTGGGCGCCTTATGGACTTCTGCTGGAGGTGCAGGCTGCC	2340
Db	2425 CCTCTGCACTGCGCTGTGGGCGCCTTATGGACTTCTGCTGGAGGTGCAGGCTGCC	2484
Qy	2341 GTGCCCGGCTCTGCCAGCCGGTGAAAGTGTGGCAGTCCGGCCAGCTCCAGGGCTCAGC	2400
Db	2485 GTGCCCGGCTCTGCCAGCCGGTGAAAGTGTGGCAGTCCGGCCAGCTCCAGGGCTCAGC	2544
Qy	2401 ATCTTTGACAGGACCTGCGCTCTGCCATGGATGAGGCCCTCTCTGGACTGTTTCGCC	2460
Db	2545 ATCTTTGACAGGACCTGCGCTCTGCCATGGATGAGGCCCTCTCTGGACTGTTTCGCC	2604
Qy	2461 CTCTCGCTGGCTGTGGCTCTGGCCATGGCCATGCTGCATCACCTCTGTGGC	2520
Db	2605 CTCTCGCTGGCTGTGGCTCTGGCCATGGCCATGCTGCATCACCTCTGTGGC	2664
Qy	2521 TGGGACCTCTGGTACTGGCTCCACCTGTGCCCTGGCTTCCCCTGGCGGGGGCGCAA	2580
Db	2665 TGGGACCTCTGGTACTGGCTCCACCTGTGCCCTGGCTTCCCCTGGCGGGGGCGCAA	2724
Qy	2581 AGTGGGCGAGATGAGGATGCCCTGCCCTACGATGCCCTCGATGGCTTCGACAAAACGCAG	2640
Db	2725 AGTGGGCGAGATGAGGATGCCCTGCCCTACGATGCCCTCGATGGCTTCGACAAAACGCAG	2784
Qy	2641 AGCGCAGTGGCAGACTGGGTGTACAACGAGCTTGGGCCAGCTGGAGGAGTGGCTGGG	2700
Db	2785 AGCGCAGTGGCAGACTGGGTGTACAACGAGCTTGGGCCAGCTGGAGGAGTGGCTGGG	2844
Qy	2701 CGCTGGGCACTCCGCTGTGCCCTGGAGGAACGCAGCTGGCTGCCCTGGCAAAACCTCTT	2760
Db	2845 CGCTGGGCACTCCGCTGTGCCCTGGAGGAACGCAGCTGGCTGCCCTGGCAAAACCTCTT	2904
Qy	2761 GAGAACCTGTGGGCTCGGTCTATGGCAGCCGAAGACGCTGTTGTGCTGGCCACACG	2820
Db	2905 GAGAACCTGTGGGCTCGGTCTATGGCAGCCGAAGACGCTGTTGTGCTGGCCACACG	2964
Qy	2821 GACCGGGTCAGTGGTCTTGCGCCAGCTTCTGCTGGGCCAGCAGCGCCTGCTGGAG	2880
Db	2965 GACCGGGTCAGTGGTCTTGCGCCAGCTTCTGCTGGGCCAGCAGCGCCTGCTGGAG	3024
Qy	2881 GACCGCAAGGACGTGGTGTGGTGTGGTGTCTGAGCCCTGACGGCCGCCCTCCCGTAC	2940
Db	3025 GACCGCAAGGACGTGGTGTGGTGTGGTGTCTGAGCCCTGACGGCCGCCCTCCCGTAC	3084
Qy	2941 GTGCCGGCTGGCCAGGCCCTGCCAGAGTGTCTCTCTGCCCCACCAGCCAGT	3000
Db	3085 GTGCCGGCTGGCCAGGCCCTGCCAGAGTGTCTCTCTGCCCCACCAGCCAGT	3144
Qy	3001 GGTCAGCGCAGCTTCTGGGCCAGCTGGGATGGCCCTGACCGAGGACAACCACTTC	3060
Db	3145 GGTCAGCGCAGCTTCTGGGCCAGCTGGGATGGCCCTGACCGAGGACAACCACTTC	3204
Qy	3061 TATAACCGGAACCTCTGCCAGGGACCCACGGCGAA	3096
Db	3205 TATAACCGGAACCTCTGCCAGGGACCCACGGCGAA	3240